



#8

032301.218.ST25.txt
SEQUENCE LISTING

<110> BATHE, Brigitte, et al.
<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ppkK GENE
<130> 032301 WD 218
<160> 2
<170> PatentIn version 3.1
<210> 1
<211> 1239
<212> DNA
<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> (237)..(1022)
<223>

BEST AVAILABLE COPY

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60

a' accggatcga ctgtcgaact tttggtgttg gtgtagtccc acaaattggt gagttcagca 1
20

cgcttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcacgcaac 1
80

tcattaaacg attgttggtc cataagacca tcatcgttgt ttttttagaa aattgc ctg 2
39

Met

1

cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga 2
87

Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly

5

10

15

ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac 3

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35

Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn

20

25

30

ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct

83

3

Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro

35

40

45

aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att

31

4

Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile

50

55

60

65

tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcg gtc

79

4

Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val

70

75

80

gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg

27

5

Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp

85

90

95

atc ggc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat ggc cga

75

5

Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg

100

105

110

gag atc acc gtt ctc aat gac gca gac gcc gcc ggc atc gcc gaa gca

23

6

Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu Ala

115

120

125

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acc ttt ggc aac cct gcc gca cgc gaa ggc gca gtc atc ctg ctg acc 6
71

Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu Thr

130 135 140 145

ctt ggt aca ggt att gga tcc gca ttc ctt gtg gat ggc caa ctg ttc 7
19

Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu Phe

150 155 160

ccc aac aca gaa ctc ggt cac atg atc gtt gac ggc gag gaa gca gaa 7
67

Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala Glu

165 170 175

cac ctt gca gca gca tcc gtc aaa gaa aac gaa gat ctg tca tgg aag 8
15

His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp Lys

180 185 190

aaa tgg gcg aag cac ctg aac aag gtg ctg agc gaa tac gag aaa ctt 8
63

Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys Leu

195 200 205

ttc tcc cca tcc gtc ttc atc atc ggt ggc gga att tcc aga aag cac 9
11

Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys His

210 215 220 225

gaa aag tgg ctt cca ttg atg gag cta gac act gac att gtc cca gct 9
59

Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro Ala

230 235 240

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gag ctg cgc aat cga gcc gga atc gta gga gct gcc atg gca gta aac 10
07

Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val Asn

245

250

255

caa cac ctc acc cca taagttatcg aaaggtgatt ttgcccagg gccttgattc 10
62

Gln His Leu Thr Pro

260

acaacgcacc ttgctgtagg aaaaacaggc ccctttgtga catcggcgta gttgttcaac 11
22

tataatggaa cgctgatcgt ggacaagagt taaccatgag attgattcac ccctttaagc 11
82

ctccaaagaa gtagttgact caacgcattt cggcatttaa aaaagccgag agcaaat 12
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<210> 2

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

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20 25 30

Asn Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr
35 40 45

Pro Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile
50 55 60

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Ile Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser
65 70 75 80

Val Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser
85 90 95

Trp Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly
100 105 110

Arg Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu
115 120 125

Ala Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu
130 135 140

Thr Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu
145 150 155 160

Phe Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala
165 170 175

Glu His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp
180 185 190

Lys Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys
195 200 205

Leu Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys
210 215 220

His Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro
225 230 235 240

Ala Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val
245 250 255

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a) Asn Gln His Leu Thr Pro
260

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